

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: December 3, 2000, 10:15:10 : Search time 10069.4 Seconds  
(without alignments)  
3787.874 Million cell updates/sec

Title: US-09-227-881-3

Perfect score: 6169

Sequence: 1 atcttgtagctggttaacctc.....ctgtgccccctccatgtag 6169

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 7189864 seqs, 3091403243 residues

Total number of hits satisfying chosen parameters: 14379728

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_est4:\*  
5: gb\_est5:\*  
6: gb\_est6:\*  
7: gb\_est7:\*  
8: gb\_est8:\*  
9: gb\_est9:\*  
10: gb\_est10:\*  
11: gb\_est11:\*  
12: gb\_est12:\*  
13: gb\_est13:\*  
14: gb\_est14:\*  
15: gb\_est15:\*  
16: gb\_est16:\*  
17: gb\_est17:\*  
18: gb\_est18:\*  
19: gb\_est19:\*  
20: gb\_est20:\*  
21: gb\_est21:\*  
22: gb\_est22:\*  
23: gb\_est23:\*  
24: gb\_est24:\*  
25: gb\_est25:\*  
26: gb\_est26:\*  
27: gb\_est27:\*  
28: gb\_est28:\*  
29: gb\_est29:\*  
30: gb\_est30:\*  
31: gb\_est31:\*  
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34: gb\_est34:\*  
35: gb\_est35:\*  
36: gb\_est36:\*  
37: gb\_est37:\*  
38: gb\_est38:\*  
39: gb\_est39:\*  
40: gb\_est40:\*  
41: em\_est4a:\*  
42: em\_estfun:\*  
43: em\_esthum1:\*

44: em\_esthum2:\*  
45: em\_esthum3:\*  
46: em\_esthum4:\*  
47: em\_esthum5:\*  
48: em\_esthum6:\*  
49: em\_esthum7:\*  
50: em\_esthum8:\*  
51: em\_esthum9:\*  
52: em\_esthum10:\*  
53: em\_esthum11:\*  
54: em\_esthum12:\*  
55: em\_esthum13:\*  
56: em\_esthum14:\*  
57: em\_esthum15:\*  
58: em\_esthum16:\*  
59: em\_esthum17:\*  
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61: em\_esthum19:\*  
62: em\_esthum20:\*  
63: em\_estin1:\*  
64: em\_estin2:\*  
65: em\_estin3:\*  
66: em\_estin4:\*  
67: em\_estom:\*  
68: em\_estov1:\*  
69: em\_estov2:\*  
70: em\_estp1:\*  
71: em\_estp12:\*  
72: em\_estp13:\*  
73: em\_estp14:\*  
74: em\_estp15:\*  
75: em\_estp16:\*  
76: em\_estro1:\*  
77: em\_estro2:\*  
78: em\_estro3:\*  
79: em\_estro4:\*  
80: em\_estro5:\*  
81: em\_estro6:\*  
82: em\_estro7:\*  
83: em\_estro8:\*  
84: em\_estro9:\*  
85: em\_estro10:\*  
86: em\_estro11:\*  
87: em\_estro12:\*  
88: em\_estro13:\*  
89: gb\_gss1:\*  
90: gb\_gss2:\*  
91: gb\_gss3:\*  
92: em\_gss4:\*  
93: em\_gss1:\*  
94: em\_gss2:\*  
95: em\_gss3:\*  
96: em\_gss4:\*  
97: gb\_gss5:\*  
98: gb\_gss6:\*  
99: gb\_gss7:\*  
100: gb\_gss8:\*  
101: gb\_gss9:\*  
102: gb\_gss10:\*  
103: gb\_gss11:\*  
104: gb\_gss12:\*  
105: gb\_gss13:\*  
106: gb\_gss14:\*  
107: gb\_gss15:\*  
108: gb\_gss16:\*  
109: gb\_gss17:\*  
110: gb\_gss18:\*  
111: gb\_gss19:\*  
112: gb\_gss20:\*  
113: gb\_gss21:\*  
114: gb\_gss22:\*  
115: gb\_gss23:\*  
116: gb\_gss24:\*  
117: em\_gss5:\*





Accession: AQ387027  
Version: AQ387027.1  
GI: 4358050  
Source: GSS.  
Organism: Homo sapiens  
Reference: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 678)  
Authors: Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter, J.C.  
Title: Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building  
Journal: Unpublished (1997)  
Comment: Other GSS: RPCI11-153C12.TV  
Contact: Shaying Zhao, William Nierman, Mark Adams  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: hbeet@igr.org  
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@ed.jong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tldb/humgen/bac\_end\_search/bac\_end\_search.html  
Seq primer: Sp6  
Class: BAC ends.

FEATURES  
source  
1..678  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/db\_xref="taxon:9606"  
/clone\_lib="RPCI-11-153C12"  
/clone\_1b="RPCI-11"  
/sex="Male"  
/cell\_type="Lymphocytes"  
/note="Vector: PBAC3.6; Site\_1: EcoRI; Site\_2: EcoRI; RPCI11 Human Male BAC Library"

BASE COUNT  
210 a 151 c 171 g 146 t

ORIGIN

Query Match  
Best Local Similarity 77.4%; Score 179; DB 96; Length 678; Pred. No. 7.9e-22; Mismatches 60; Indels 8; Gaps 1; Matches 233; Conservative 0;

1274 tccgtgagggtagggctgtgtcttaaccctctgtatgtctacacgtgagctact 1333  
1334 gcaacctctgctcccaaggtcaagcaattctctgtctcaagcctcccgctagctgga 1393  
1394 ctaaacgc-----gcaagcccgctaatcttctgtatgtctagtagagatgggtcttc 1445  
1446 accatattagccggctggtcttgaactctgaactcaaggtgataccacccacccctcagcct 1505  
1506 cctaaagtctgtaggattacaggaatgacccgcccgcacaaaggtcagtgcttaatt 1565  
1566 a 1566  
64 A 64

Result: 5  
Accession: AM978041  
Version: EST390150  
Source: MAGE resequences, MAGO  
Organism: Homo sapiens  
Reference: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 537)  
Authors: Hegde, P., Qi, R., Abernathy, K., Dharp, S., Gaspard, R., Gay, C., Holt, I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and Quackenbush, J.  
Title: Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray  
Journal: Unpublished (2000)  
Comment: Contact: John Quackenbush  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 3528  
Fax: 301 838 0208  
Email: johng@tigr.org  
Plate: 387  
Seq primer: Forward.

FEATURES  
source  
1..537  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="MAGE resequences, MAGO"  
/note="Vector: pBluescriptSk"

BASE COUNT  
119 a 157 c 141 g 118 t 2 others

ORIGIN

Query Match  
Best Local Similarity 77.2%; Score 178.4; DB 25; Length 537; Pred. No. 1e-21; Mismatches 61; Indels 8; Gaps 1; Matches 233; Conservative 0;

1281 gggtaggggtctgtgtcttaaccctctgtatgtctctacacgtgagctcagcact 1340  
1341 ctgctctcccaaggtcaagcaattctctgtcttagcctcccggtgagctcagcact 1400  
1401 cg-----cagcccggtcaattcttctgtatgtcttagtagagatgggtctcaacat 1452  
1453 tagccggctggtctgaactctgaactcctgaagtgatgacacccacccctcagcctc 1512  
1513 tgctggattacaggcagctacccgcccgcacaaaggtcagtgcttaataaaggaa 1572  
1573 aa 1574  
306 AA 307

RESULT 6  
LOCUS: AQ112451 516 bp DNA  
DEFINITION: CIT-HSP-2372C9.TF CIT-HSP Homo sapiens genomic clone 2372C9, DNA sequence.  
ACCESSION: AQ112451  
VERSION: AQ112451.1 GI: 3484611

KEYWORDS	GSS.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homin.
AUTHORS	1 (bases 1 to 516) Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.
TITLE	Use of a random human BAC End Sequence Database for Sequence-Ready Map Building
JOURNAL	Unpublished (1998)
COMMENT	Other_GSS: CIT-HSP-2372C9.TR Contact: Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: mdadams@tigr.org Clones are available from Research Genetics (info@resgen.com). BAC end search page: <a href="http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html">http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html</a> . Seq primer: M13-21 Class: BAC ends.
FEATURES	Location/Qualifiers 1..516 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="2372C9" /clone_lib="CIT-HSP" /sex="Male" /cell_type="Sperm" /note="Vector: pBeloBAC11; site_1: HindIII; site_2: HindIII"
BASE COUNT	87 a 145 c 118 g 166 t
ORIGIN	
Query Match	2.9%; Score 177.6; DB 89; Length 516; Best Local Similarity 85.2%; Pred. No. 1.4e-21;
Matches 213; Conservative 0; Mismatches 29; Indels 8; Gaps 1	
OY 1321	accctgagctcactgcgaacctctgcctcccaaggttcaagaatctctcgtctcaagctcc 1380
DB 255	ANCTGACGTCACTGCACACTCTGCGTCCCGGGTTCAAGCATCTCTCGTCAAGCCTCC 314
OY 1381	cgcgtagctcgggaactaagcg-----caagcccggttaattttgtatgttagta 1432
DB 315	CAGTAGCGTGGGATTAACAGCGCACACACACACAGCCCGGCTAATTTTATTATTAAATA 374
OY 1433	gagatggaggtttcacacatatagccgagctgtgctctgaactcctgaccctcaagtgatca 1492
DB 375	GAGATGGGGTTTACACCATTTTGCGCCAGGCTGGTCTGAACCTCTGACCTTAGGTATCCA 434
OY 1493	cccaactcagacctctcaagtgctggatattacagcagatagtcacccgcgcgcgccaagg 1552
DB 435	CCCACTTGCGCTCCCAAGAAGTGTGGATTAACAGCGCTGGCCACATGCGCCAGCCTAAT 494
OY 1553	gtcagtgattt 1562
DB 495	TTTTGCATTT 504
RESULT 7	
AQ265389/c	577 bp DNA GSS 27-Oct-1998
LOCUS	
DEFINITION	CITBI-EI-2509010.TF CITBI-EI Homo sapiens genomic clone 2509010, DNA sequence.
ACCESSION	AQ265389
VERSION	AQ265389.1 GI:3793589
KEYWORDS	GSS.
SOURCE	human.

ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 577)
AUTHORS	Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Mable,C., Shizuya,H., Simon,M. and Venter,J.C.
TITLE	Use of a random human BAC End Sequence Database for Sequence-Ready Map Building
JOURNAL	Unpublished (1998)
COMMENT	Other.GSSE: CIBI-EI-2509010.TR Contact: Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: madams@tigr.org Clones are available from Research Genetics (info@resgen.com). BAC end search page: <a href="http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html">http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html</a> . Seq primer: M13-21 Class: Ends.
FEATURES	Location/Qualifiers 1..577 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="2509010" /clone_lib="CIBI-EI" /sex="male" /cell_type="sperm" /note="Vector: pBelOBAC11; Site_1: EcoRI; Site_2: EcoRI; Caltech Human BAC Library D"
BASE COUNT	167 a 127 c 137 g 146 t
ORIGIN	
Query Match	2.9%; Score 177.4; DB 91; Length 577;
Best Local Similarity	75.1%; Pred. No. 1.5e-21;
Matches 238; Conservative	0; Mismatches 71; Indels 8; Gaps 1;
QY	1321 acctgaagctcgaatgaacctcgcctcccaagtttaagcaatctcgcgtcccaagctcc
DB	368 ATCTGGGCTACATGGACACCTCGCTCCACAGGTTAAAGATCTCTGCTCCACAGCTTC
QY	1381 gcgcgaagctggagacacagggc-----gcacgcccgcgaatttggatgttgatga
DB	308 CGAGTATCTAGAGACATACAGGACACCGCCACACAGGCTGGCTAATTTTGGTATTTAGTA
QY	1433 ggaatgagggtttacacatatatagcccgagcttggtcttgaacctcgaacctcagtgatca
DB	248 GAGAGGGGGTTTACACCATGTTGTGTCAGGCTGGTCTTGAACCTCTGACCTCAGGCGATCCA
QY	1493 cccacactcagcctcctctaaagtctcgtgatttaagagcatgagtcacccgccccggcgaag
DB	188 CCCGGCTTGGCTCCCAAGTGCTGGGATTAAGGCATAGGCCACTGCACCCAGCCAGCA
QY	1553 gtcagtgatttaaggaataactggaatggttactaacaacacagaggaagacagacaaa
DB	128 GATACATTTTGTAAATCTAGACTGGAGTCACTGGACAGACTCTCTCAGGCAAAAGGAGAA
QY	1613 agctgtgataaatttcag 1629
DB	68 AGTAATTAAGTGTATGAG 52
RESULT 8	
LOCUS	AI583291 548 bp mRNA EST 14-DEC-1999
DEFINITION	tt56g02.x1 NC1 CGAP_HSC4 Homo sapiens cDNA clone IMAGE:2244818 3'
ACCESSION	Similar to TR:Q13538 Q13538 ORF2: FUNCTION UNKNOWN. ; contains Alu repetitive element; mRNA sequence.

VERSION	AT583291.1	GI:4569188
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryote: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS	1 (bases 1 to 548)	
TITLE	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> . National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index	
JOURNAL	Unpublished (1997)	
COMMENT	Contact: Robert Strausberg, Ph.D. Tel.: (301) 496-1550 Email: Robert.Strausberg@nih.gov Tissue Procurement: Herbert Morse, M.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: David B. Kitzman, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <a href="http://www-bio.linnl.gov/bhrp/image/image.html">www-bio.linnl.gov/bhrp/image/image.html</a> Insert length: 664 Std Error: 0.00 Seq primer: -40UP from Gibco High quality sequence stop: 464 POLYA-No.	

```

FEATURES
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Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2244818"
/clone_1id="NCI-CGAP_HSC4"
/tissue_type="CD34+, CD38- from normal bone marrow donor"
/lab_host="DH10B"
/note="Organ: bone marrow; Vector: pMMP1; mRNA made from lymphoid tissue, cDNA made by oligo-dT priming. Directionally cloned. Size-selected on agarose gel, average insert size 500 bp. Primary library, not-amplified. cDNA library Preparation: David B. Kitzman, Ph.D. Reference: Kitzman et al. (1996) Cancer Research 56:5380-5383."
BASE COUNT
150 a 136 c 129 g 133 t
ORIGIN

```

Query Match	2.9%	Score 177.2;	DB 11;	Length 548;
Best Local Similarity	78.8%	Pred. No. 1,76-21;		
Matches 227;	Conservative 0;	Mismatches 53;	Indels 8;	Gaps 1;
Qy 1277	gtggagggatgagggatcgtgctgtgtcttaacacttaactatgctatgcttaacaccgagctactca	1336		
Db 546	GAGGAGAGCTTGAATCTGTCTGCTCAAGCGCTGGAGATGCAAGTGCATGATCTTGGCTCACTTCA	487		
Qy 1337	acctctgcctcccaagtgatcaagaatctccatgtctcagccctccgcgtaagctggagacta	1396		
Db 486	ACCTTCGGCTCTACAGGTTCACAGCAATTTCTCTGCTCCAGCTCCAGACACTGTGAGATTA	427		
Qy 1397	cagggcg-----cagcgccggtgaattttgtatgtgtgtagagatggggtttacc	1448		
Db 426	CAGCGCGCCCGCCACACAGCCCTGGCTGAATTTTGTATTTTATAGTAGAGTGGGATTCACC	367		
Qy 1449	atatatagcccgcgctggtcttgtaacttcctgaaacctgaagtgatgacacaccacccaagcttcc	1508		
Db 366	ATGTGGGCAAGCTGTGTGTGTGAATCTCGACCTGACCTGAGGTGATCCACCCACTTTGGATCTCC	307		
Qy 1509	aaagtgtcgtggaattacagagcatgtagtcaacgcgcgcgcgcgcgaaggtca	1556		
Db 306	AAATGCTGTGGGATTACAGCATGAGCCACCTGCGACAGCGAGATTTA	259		

RESULT	9			
AO199435/c				
LOCUS	AO199435	434 bp	DNA	GSS
				20-APR-1999

DEFINITION	RPc111-58F5.TJ RPc11-11 Homo sapiens genomic clone RPc11-58F5, DNA sequence.
ACCESSION	AO199435
VERSION	AO199435.1 GI:3611634
KEYWORDS	GSS.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 434)
AUTHORS	Berry,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Adams,K., Granger,D., Suh,E., Wible,C., de Jong,P., and Venter,J.C.
TITLE	Use of human BAC End Sequences for Sequence-Ready Map Building
JOURNAL	Unpublished (1998)
COMMENT	Other_GSSs: RPc111-58F5.TK

Contact: Mark Adams  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: [mdadams@ligr.org](mailto:mdadams@ligr.org)  
Clones are derived from the human BAC library RPC1-11. For BAC library availability, please contact Plier de Jong ([plierdejong.med.buffalo.edu](mailto:plierdejong.med.buffalo.edu)). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from Research Genetics ([info@resgen.com](http://info@resgen.com)). BAC end search page: [http://www.ligr.org/tadb/humgen/bac\\_end\\_search/bac\\_end\\_search.html](http://www.ligr.org/tadb/humgen/bac_end_search/bac_end_search.html)  
Class: BAC ends.

FEATURES	SOURCE	Location/Qualifiers
		1. 434
		/organism="Homo sapiens"
		/db_xref="GDB:7522012"
		/db_xref="taxon:9606"
		/clone="RPC1-11-58F5"
		/clone_11b="RPC1-11"
		/sex="Male"
		/cell_type="Lymphocytes"
		/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI; RPC111 Human Male BAC Library"
BASE COUNT		118 a 108 c 114 g 94 t
ORIGIN		

[illegible]

RESULT	10			
LOCUS	AM979191	591 bp	mRNA	02-JUN-2000
DEFINITION	AM979191			
	EST331301	MAGE resequences, MACP	Homo sapiens	CDNA, mRNA sequence

ACCESSION	AM979191
VERSION	AM979191.1
KEYWORDS	GI:8170478
SOURCE	EST.
ORGANISM	human. Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 381)
AUTHORS	Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt ,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and Quackenbush,J. Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray Unpublished (2000) Contact: John Quackenbush The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel.: 301 838 3528 Fax: 301 838 0208 Email: johnq@igr.org Plate: 403 Seq primer: Forward.
TITLE	Location/Qualifiers
JOURNAL	1..591
COMMENT	/organism="Homo sapiens" /db_xref="taxon:9606" /clone_1lb="IMAGE ressequences, MAGE" /note="Vector: pBluescriptSM"
FEATURES	
source	
BASE COUNT	154 a 152 c 126 g 159 t
ORIGIN	
Query Match	2.9%; Score 176.6; DB 25; Length 591;
Best Local Similarity	71.9%; Pred. No. 2..1e-21;
Matches 248:	Conservative 0; Mismatches 89; Indels 8; Gaps 1
OY	1281 gggtgaaggctcgtgtcttaacactaccctgtagtccttaacctagctactgcgaacct 1340
DB	132 GAGTCCTGCTGTCTGCACCAGCGCTGAAGTGCACATCTGGCTCCTCACGCCAACCT 191
OY	1341 ctgcctcccaagttcaagaattctccttctcagctcccgcgtagctcggaactcagg 1400
DB	192 CCACCTCCCAAGTTCAAGCAATTCTCTGTCTAAGCTCTTAAGTAGCTGGACTAGAA 251
OY	1401 cgcacg-----ccggctaaatttgatgtagttagtagagatgyggtttcacatat 1452
DB	252 GGCGCGCCACACATACCAAGATAATTTTTTCATATTTTAGTAGAGATGGGGTTCCACATAT 311
OY	1453 tagcccgctgtgtcttgaactcctgcactcgaagtgatccaaccactcgaactcctaag 1512
DB	312 TGCTCAGCGTGCTGTTGAATCTCTGCACCTCAGGTGATCCACCGCCTTGCGCTCCCAA 371
OY	1513 tgctggattcaaggatgatgctacccggcgcccgcaagggttaagtgtttaataaggaat 1572
DB	372 TCGTGGAGATGACAGGGGTAGCGCACCTGCGCCACCAACAAGTCTGGAAATTTTAGCCAA 431
OY	1573 aaactgaatcggttactaacacaacagaggaagaagaagaagctg 1617
DB	432 AATATATATCTATTTAACACTCAATGGCATTTACTCAACAAGATG 476
RESULT 11	
LOCUS	AM273360 521 bp mRNA EST 03-JUN-2000
DEFINITION	xr38a04.x1 NCL_CGAP_Ut4 Homo sapiens CDNA clone IMAGE:2762382 3'
ACCESSION	similar to contigons Alu repetitive element.; contains L1.ct L1 L1
VERSION	repetitive element.; mRNA sequence.
KEYWORDS	AM273360 GI:6660390
SOURCE	EST.
ORGANISM	human. Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT		
1 (bases 1 to 521)	Mammalia; Eutheria; Primates; Carnivora; Homiidae; Homo.	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .				
	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index	Unpublished (1997)	Contact: Robert Strausberg, Ph.D.			
	Tel: (301) 496-1550		Email: Robert.Strausberg@nih.gov			
	Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.		CGMA Library Preparation: Life Technologies, Inc.			
	CGMA Library Arrayed by: Greg Lennon, Ph.D.		DNA sequencing by: Washington University Genome Sequencing Center			
	Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILNI, at:		<a href="http://www.bio.lnlnl.gov/bbrp/image/image.html">www.bio.lnlnl.gov/bbrp/image/image.html</a>			
FEATURES	source	location/Qualifiers	1..521			
	Possible reversed clone: polyr not found					
	Seq primer: -400P from Gibco					
	High quality sequence stop: 411.					
BASE COUNT	ORIGIN	115 a	131 c	108 g		
				167 t		
Query Match	2.9%	Score 176;	DB 21;	Length 521;		
Best Local Similarity	80.7%	Pred. No. 2.7e-21;				
Matches 221; Conservative	0;	Mismatches 45;	Indels 8;	Gaps 1;		
QY 1321	acctgagcctcatgtgaacctctgctccaggtttaagaatctctcgtctcaagctcc			1380		
DB 56	ATCTGGGCTCACTGCAACCTGCTCCCAAGTTCAGGATTCCTGCTCAGCCTCC			115		
QY 1381	cgcgtgctcgtggaaccaagcg-----cagcccgccctaattttgattgtttagta			1432		
DB 116	TGAGTACGACGAGATTCACAGGTGCTCCGACACACACACACACATATTTTGTATTTTAGTA			175		
QY 1433	gagatgaggttaccataatagcccggtgtgtcttgaaaccttgacctcaagtgatcca			1492		
DB 176	GAGATGGGTTTACATATGTTGGCAGGCTAGTCTTGTACTCTGACCTCAGAGTATCCA			235		
QY 1493	cccaactcagcctcctaaagtgtctggatattcaggacatgagtcacccgcccggccaag			1552		
DB 236	CCCGCTCAGCTCCCAAGGCTGTGGGATTAACAGGATGATGACACGCCCTGCGCTTTC			295		
QY 1553	gtcagtggttaataaggaataactgtgaatgttt			1586		
DB 296	CTGACTTTTACTGATCACCATTCTACTGATAT			329		
RESULT 12	LOCUS	T53829	551 bp	mRNA	EST	06-FEB-1995
	DEFINITION	YB85d10.s1	Stratagene liver (#937224)	Homo sapiens cDNA clone		
	IMAGE:7791	3	similar to contains 11	repetitive element, mRNA		
	sequence.					
	ACCESSION	T53829				
	VERSION	EST.	GI:655690			
	KEYWORDS					
	SOURCE			human.		

ORGANISM	Homo sapiens
REFERENCE	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Primates: Catarrhini: Homnidae: Homo. 1 (bases 1 to 551)
AUTHORS	Hallier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissee, S., Dietrich, N., Dubuque, T., Favell, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevas, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
TITLE	Washington University School of Medicine
JOURNAL	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
MEDLINE	Tel: 314 286 1800
COMMENT	Fax: 314 286 1810 Email: est@watson.wustl.edu Insert Size: 760 High quality sequence stops: 380 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 760 Std Error: 0.00 Seq primer: -21ml3 High quality sequence stop: 380. Location/Qualifiers 1. 551 /organism="Homo sapiens" /db_xref="GDB:497716" /db_xref="taxon:9606" /clone="IMAGE:77971" /clone_11b="Stratagene liver (#937224)" /sex="male" /dev_stage="49 years old" /lab_host="SODR cells (kanamycin resistant)" /note="Organ: liver; Vector: pBluescript SK; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Hepatectomy from normal male caucasian. Average insert size: 1.1 kb; Uni-ZAP XR Vector: -5' adaptor sequence: 5' GAATTCGCCACGAC 3' -3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTTCTTTT 3'."
BASE COUNT	119 a 134 c 127 g 163 t 8 others
ORIGIN	
Query Match	2.9% Score 176; DB 39; Length 551;
Best Local Similarity	80.7% Pred. No. 2.7e-21;
Matches 221; Conservative	0; Mismatches 45; Indels 8; Gaps 1;
Oy 1321	accgagctcactgcaactctgctccaggttcaagcaattcctctcagccctc 1380
Db 47	ATTCGCTCACTGCACTCTGCTCCAGATTCAGATTCCTGCTCAGCTCC 106
Oy 1381	cgctgagctggaactagcg-----cagcgccgagctaatltgtatgttga 1432
Db 107	TGAGTAGCAGGAGATTAACGAGGCCCGCACCAACAGCTAATTTTGTATTACTA 166
Oy 1433	gagatgaggttccaccataatagcccgctgcttgaactccggaactcaggtatcca 1492
Db 167	GAGATGGGGTTTCACTAGTTGGCCAGGCTAGTCTTTACTCTGACCTCAGGTGATCA 226
Oy 1493	cccccctcagctctcctaaagctgctgaggttcaagagcatgagtcacggcgcccaag 1552
Db 227	CCCCGCTAGCCTCCCAAGAGTGCTGGGATTACAGGCAATGAGTCAACGCCCTGGCCTTTC 286
Oy 1553	gtcaggttttaataagagataactgtaagttc 1586
Db 287	CTGACTTTTAGTGTATCACAATTCTAAGTAT 320
RESULT 13	
AO283440	

LOCUS	AO283440 589 bp DNA GSS 27-APR-1999
DEFINITION	RPc11-79G5.TJ RPc1-11 Homo sapiens genomic clone RPc1-11-79G5, DNA sequence.
ACCESSION	AO283440
VERSION	AO283440.1 GI:3908257
KEYWORDS	GSS.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Primates: Catarrhini: Homnidae: Homo. 1 (bases 1 to 589)
AUTHORS	Adams, M.D., Rounsley, S.D., Zhao, S., Baas, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C. Use of human BAC End sequences for sequence-ready map building Unpublished (1998)
TITLE	Unpublished (1998)
JOURNAL	Other GSSs: RPc11-79G5.TJ
COMMENT	Contact: Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: mdamadms@tigr.org Clones are derived from the human BAC library RPc1-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.bufileo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.bufileo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.html Seq primer: SP6 Class: BAC ends. Location/Qualifiers 1. 589 /organism="Homo sapiens" /db_xref="GDB:7530100" /db_xref="taxon:9606" /clone="RPc1-11-79G5" /clone_11b="RPc1-11" /sex="male" /cell_type="lymphocytes" /note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI; RPc111 Human Male BAC Library"
BASE COUNT	146 a 126 c 136 g 181 t
ORIGIN	
Query Match	2.8% Score 175.8; DB 91; Length 589;
Best Local Similarity	75.7% Pred. No. 2.9e-21;
Matches 234; Conservative	0; Mismatches 67; Indels 8; Gaps 1;
Oy 1280	agggtgagggctgtgtcttaacactcgtatgctcctacacctgagctcaatgcaacc 1339
Db 105	AGAGTCTTGTCTCTGTGGCCAGGCTGAGTACAGTGGATGATTCAGCTCAGCAACC 164
Oy 1340	tctgctcccaaggttcaagaatctcctgtctcagctcccgctagctcgtggaactacg 1399
Db 165	TCTACATCTCTGGTTCAAGCAATCTCTGCTTAGCCGCCCGAGTGTGAGTTTACAG 224
Oy 1400	gctg-----cagcccgctaatlttgtatgttagtagagatgaggtttaccata 1451
Db 225	GTCGCTCCACCAAGCTTACTAATTTTATTTTATTTTATTTTATTTTATTTTATTTT 284
Oy 1452	ttaacccgagctgctgctgaactcctgaccccaaggtgatacccaactcagcctctaa 1511
Db 285	TTGATCAGGCTGCTGTGAACTCTGTACCTCATGTATGATCCACCGTTCAGCCCTCAAA 344
Oy 1512	gtgtgtgagttacagagcatgataccgctccgcccgaaggttcaaggttttaagaa 1571
Db 345	GTCTGGAGTATACAGGCGTGTGAGCCAGCTGCTGCTCAGAGGGATGATTTTATAGAA 404
Oy 1572	ttaactgaa 1580
Db 405	TAAATGTCA 413



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RESULT 14
LOCUS AO474222/c
DEFINITION AO474222 386 bp DNA GSS 23-Apr-1999
CITBI-EI-2601EI18.TR CITBI-EI Homo sapiens genomic clone 2601EI18,
DNA sequence.
ACCESSION AO474222
VERSION AO474222.1 GI:4652483
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
            Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 366)
AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
            Venter,J.C.
TITLE Use of BAC End Sequences from Caltech Libraries for Sequence-Ready
            Map Building
            Unpublished (1997)
JOURNAL Other GSSs: CITBI-EI-2601EI18.TF
COMMENT Contact: Shaying Zhao, William Nierman, Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: hbeetlgr.Org
            Clones are available from Research Genetics (info@resgen.com). BAC
            end search page:
            http://www.tigr.org/cdb/hungen/Bac_end_search/Bac_end_search.html.
            Seq primer: M13 Reverse
            Class: BAC ends.

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FEATURES	SOURCE	Location/Qualifiers
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		/clone_1b="CITb1-E1"
		/sex="male"
		/cell_type="sperm"
		/note="Vector: pBelbac11; Site_1: EcoRI; Site_2: EcoRI;
		Caltech Human Bac Library D"
BASE COUNT		88 a 104 c 116 g 78 t
ORIGIN		

[illegible]

LOCUS	AOA15030/c				
DEFINITION	AOA15030	711 bp	DNA	GSS	23-MAR-1999
ACCESSION	RPCI-11-203E3.TV	RPCI-11	Homo sapiens	genomic clone	RPCI-11-203E3,
VERSION	AOA15030				
KEYWORDS	DNA sequence.				
SOURCE	AOA15030.1	GI:4473999			
ORGANISM	GSS.				
	human.				
	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
REFERENCE	1 (bases 1 to 711)				
AUTHORS	Zhao, S., Adams, M.D., Niernman, W., Malek, J., de Jong, P. and Venter, J.C.				
TITLE	Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready				
JOURNAL	Map Building				
COMMENT	Unpublished (1997)				
	Other-GSSs: RPCI-11-203E3.TJ				
	Contact: Shaying Zhao, William Niernman, Mark Adams				
	Department of Eukaryotic Genomics				
	The Institute for Genomic Research				
	9712 Medical Center Dr., Rockville, MD 20850				
	Tel: 301 838 0200				
	Fax: 301 838 0208				
	Email: hdbet@tigr.org				
	Clones are derived from the human BAC library RPCI-11. For BAC				
	library availability, please contact Plieter de Jong				
	(plieter@ejong.med.buffalo.edu). Clones may be purchased from				
	BACPAC Resources ( <a href="http://bacpac.med.buffalo.edu/ordering">http://bacpac.med.buffalo.edu/ordering</a> ) or from				
	Research Genet cs ( <a href="mailto:info@resgen.com">info@resgen.com</a> ). BAC end search page:				
	<a href="http://www.tigr.org/tcdb/humgen/bac_end_search/Bac_end_search.html">http://www.tigr.org/tcdb/humgen/bac_end_search/Bac_end_search.html</a> .				
	Seq primer: T7				
	Class: BAC ends.				

FEATURES	SOURCE	location/Qualifiers
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		/organism="Homo sapiens"
		/db_xref="GDB:757766"
		/db_xref="taxon:9606"
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		/clone_1lb="RPC1-11"
		/sex="Male"
		/cell_type="Lymphocytes"
		/note="Vector: pBac3.6; Site_1: EcoRI; Site_2: EcoRI"
		RPC11 Human Male BAC Library"
BASE COUNT		270 a 150 c 141 g 150 t
ORIGIN		

Query Match	2.8%	Score 175.2	DB 97	Length 711
Best Local Similarity	74.5%	Pred. No. 3.7e-21		
Matches 237	Conservative	0	Mismatches 73	Indels 8
				Gaps 1
QY 1281	gggttagggctctgtgctctacacacactctgatctctacaccttgagctcattgcaacct	1340		
DB 365	GAGTCTTGCTCTGTCTGCCCGAGGCTGGAGTGCAGTGGCATGATCTCGGCTCATGCAAACT	306		
QY 1341	ctgctctcccaaggttcaagaacattctctgtctccagcctcccggttagcttgagcttaacgg	1400		
DB 305	CCGGCTCCCGGTTCAAGCAATTCTCGTCTCAGCCCTCCGAGTACTCGGATTCACAG	246		
QY 1401	cgcac-----gcccgctaatcttgattgtttgttagtagaga ttgggttccacat	1452		
DB 245	TGCAACCTACGATGCCACCTAATTTTGTATTTTATATAGAAAGGGTTTCTCCATCT	186		
QY 1453	tacccggctcgtgtcttgaacctccctgacctcaggtgatgtacacccacacctcaagcttaag	1512		
DB 185	TGGCCAGGCTGGTCTTGAACCTCTACCTCAGTGATCCGGCAGCCTCAGAGCTCCCAAAG	126		
QY 1513	tgcctggattatcagcagcatagttacccggcccgcccaagggttcagtgctttaataaggaat	1572		
DB 125	TGCTGGAAATTACAGGATGAGCCACTGTGCTCCGCGCTATAGTTTTCATTTCTTATGATAT	66		
QY 1573	aacttgaatggttacta	1590		

Db 65 CTTCTCTGCTTTCGTA 48

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Job time: 14004 sec

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